Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of Claims:

Claims 1-44. **(Cancelled)**

Claim 45. **(Currently Amended)** A method of detecting an amplification or gain of unique sequences at at least one chromosomal region selected from the group consisting of:

on human chromosome 1,
about position p22 to the centromere;
the q arm;
the centromere to about position p32;
about position q31 to qter;
about position q32;
about position q32 to qter;
on human chromosome 2,
the p arm;
on human chromosome 3,
about position p14;
about position p14 to qter;
about position p22 to pter;
about position q26 to qter;
on human chromosome 4,

the p arm;

about position q32 to about position q34;

on human chromosome 5,

the p arm;

about position q31 to qter;

about position q32 to qter;

on human chromosome 6,

the p arm;

the centromere to about position p21;

about position p23 to pter;

the centromere to about position q21;

about position q12 to about position q13;

about position q21;

about position q21 to about position q22;

on human chromosome 7,

the p arm;

the centromere to about position p12;

about position p21;

pter to about position q31;

the q arm;

about position q22 to about position q32;

on human chromosome 8,

about position p12;

the q arm;

about position q21;

about position q21 to about position q23;

about position q21 to qter;

about position q22 to about position q23;

about position q22 to qter;

about position q23 to about position q24;

about position q23 to qter;
about position q24;
on human chromosome 10,
the p arm;
the centromere to about position q21;
about position q22;
on chromosome 11,
about position p15;
the q arm;
about position q13;
on human chromosome 12,
the p arm;
the q arm;
about position q14 to about position q15;
about position q21;
about position q21 to about position q23;
about position q24;
on human chromosome 13,
about position 22 to qter;
about position q31 to qter;
on human chromosome 14,
the q arm;
about position q24 to qter;
about position q31;
about position q31 to qter;
on human chromosome 15,
about position q21 to qter;
about position q24;
about position q25;
about position q26;

entire human chromosome 16;

on human chromosome 16,

the p arm;

the q arm;

about position q23 to about position q24;

on human chromosome 17,

the centromere to about position q24;

about position q12;

about position q21 to qter;

about position q22 to about position q23;

about position q22 to about position q24;

about position q22 to qter;

about position q24 to qter;

on human chromosome 18,

the p arm;

on human chromosome 19,

the q arm;

about position q13;

about position q13 to qter;

entire human chromosome 20;

on human chromosome 20,

the p arm;

the q arm;

about position q12 to about position q13;

about position q13;

about position q13 to qter;

about position q34;

qter;

entire chromosome 21;

entire chromosome 22;

on the human X chromosome,

the p arm,

in a test sample, said method comprising:

(a) labelling nucleic acids from the test sample and from a control sample with different labels;

(b) contacting said labelled nucleic acids from each sample with a plurality of target nucleic acids, wherein either the labelled nucleic acids or the target nucleic acids, or both, have had repetitive sequences, if initially present, blocked and/or removed; and

(c) comparing the intensities of the signals from labelled nucleic acids hybridized to each target nucleic acid, thereby allowing detection of the presence or absence of the gain or amplification [or gain] in the test sample.

Claim 46. **(Previously Presented)** The method of claim 45, wherein the step of comparing the intensities of the signals from the labelled nucleic acids comprises determining the ratio of the intensities of the signals as a function of position in the target nucleic acids.

Claim 47. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 1.

Claim 48. **(Previously Presented)** The method of claim 45, wherein the amplification is of the p arm of human chromosome 7.

Claim 49. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 8.

Claim 50. **(Previously Presented)** The method of claim 45, wherein the amplification is at about position q24 on human chromosome 8.

Claim 51. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 11.

Claim 52. **(Previously Presented)** The method of claim 45, wherein the amplification is at about position q13 on human chromosome 11.

Claim 53. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 12.

Claim 54. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 14.

Claim 55. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 16.

Claim 56. **(Previously Presented)** The method of claim 45, wherein the amplification is at about position q22 to about position q24 on human chromosome 17.

Claim 57. **(Previously Presented)** The method of claim 45, wherein the amplification is of the q arm of human chromosome 20.

Claim 58. **(Previously Presented)** The method of claim 45, wherein the target nucleic acids comprise at least one metaphase chromosome.

Claim 59. **(Previously Presented)** The method of claim 45, wherein said nucleic acid sample comprises genomic DNA molecules.

Claim 60. **(Previously Presented)** The method of claim 45, wherein said nucleic acid sample comprises DNA amplified from said test sample.

Claim 61. **(Previously Presented)** The method of claim 45, wherein said nucleic acid sample comprises complementary DNA.

Claim 62. **(Re-presented)** A method of detecting a deletion of unique sequences at at least one chromosomal region selected from the group consisting of:

on human chromosome 9, the p arm;

on human chromosome 16,

the q arm;

about position q22;

on human chromosome 17, the p arm;

in a test sample, said method comprising:

(a) labelling nucleic acids from the test sample and from a control sample with different labels;

(b) contacting said labelled nucleic acids from each sample with a plurality of target nucleic acids, wherein either the labelled nucleic acids or the target nucleic acids, or both, have had repetitive sequences, if initially present, blocked and/or removed; and

(c) comparing the intensities of the signals from labelled nucleic acids hybridized to each target nucleic acid, thereby allowing detection of the presence or absence of the deletion in the test sample.

Claim 63. **(Re-presented)** The method of claim 62, wherein the step of comparing the intensities of the signals from the labelled nucleic acids comprises determining the ratio of the intensities of the signals as a function of position in the target nucleic acids.

Claim 64. **(Re-presented)** The method of claim 62, wherein the target nucleic acids comprise at least one metaphase chromosome.

Claim 65. **(Re-presented)** The method of claim 62, wherein said nucleic acid sample comprises genomic DNA molecules.

Claim 66. **(Re-presented)** The method of claim 62, wherein said nucleic acid sample comprises DNA amplified from said test sample.

Claim 67. **(Re-presented)** The method of claim 62, wherein said nucleic acid sample comprises complementary DNA.

Claim 68. **(Currently Amended)** A method for detecting a copy number variation in a suspected breast cancer sample by detecting a gain of an entire chromosome or chromosome arm or an amplification [or gain] of unique sequences at at least one chromosomal region, wherein said entire chromosome, chromosome arm, or chromosomal region is selected from the group consisting of:

on chromosome 17, about position q22 to about position q24;
on chromosome 20,
the q arm;
about position q13,
said method comprising:

(a) contacting a probe that binds selectively to a target polynucleotide sequence of said region with a nucleic acid sample prepared, directly or indirectly, from said suspected breast cancer sample, wherein said nucleic acid sample comprises said target polynucleotide sequence and said probe is contacted with said sample under conditions in which said probe forms a stable hybridization complex with said target nucleic acid sequence; and

(b) detecting said hybridization complex.

Claim 69. **(Previously Presented)** The method of claim 68, wherein said probe is labeled.

Claim 70. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample is labeled.

Claim 71. **(Previously Presented)** The method of claim 68, wherein the amplification is at about position q22 to about position q24 on human chromosome 17.

Claim 72. **(Withdrawn)** The method of claim 68, wherein the amplification is of the q arm of human chromosome 20.

Claim 73. **(Withdrawn)** The method of claim 68, wherein the amplification is at about position q13 on human chromosome 20.

Claim 74. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample comprises genomic DNA molecules.

Claim 75. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample comprises DNA amplified from said suspected breast cancer sample.

Claim 76. **(Previously Presented)** The method of claim 68, wherein said nucleic acid sample comprises complementary DNA.

Claims 77-86. **(Cancelled)**